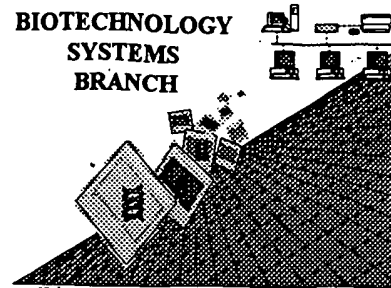


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING  
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/032,256  
Source: OIP  
Date Processed by STIC: 1/16/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,  
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,  
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/032,256

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 \_\_\_\_ Wrapped Nucleics  
    Wrapped Aminos  
    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 \_\_\_\_ Invalid Line Length  
    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 \_\_\_\_ Misaligned Amino  
    Numbering  
    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 \_\_\_\_ Non-ASCII  
    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 \_\_\_\_ Variable Length  
    Sequence(s) \_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 \_\_\_\_ PatentIn 2.0  
    "bug"  
    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 \_\_\_\_ Skipped Sequences  
    (OLD RULES)  
    Sequence(s) \_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 \_\_\_\_ Skipped Sequences  
    (NEW RULES)  
    Sequence(s) \_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9 \_\_\_\_ Use of n's or Xaa's  
    (NEW RULES)  
    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 \_\_\_\_ Invalid <213>  
    Response  
    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 \_\_\_\_ Use of <220>  
    Sequence(s) \_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 \_\_\_\_ PatentIn 2.0  
    "bug"  
    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 \_\_\_\_ Misuse of n  
    n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIEP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,256

DATE: 01/16/2002

TIME: 18:45:02

Input Set : A:\M2335hn1.app

Output Set: N:\CRF3\01162002\J032256.raw

**Does Not Comply**  
**Corrected Diskette Needed**

P.S

3 <110> APPLICANT: CHODOSH, Lewis A  
 4 GARDNER, Heather P  
 6 <120> TITLE OF INVENTION: HORMONALLY UP-REGULATED, NEU-TUMOR-ASSOCIATED KINASE  
 8 <130> FILE REFERENCE: 22253-70421  
 10 <140> CURRENT APPLICATION NUMBER: US/10/032,256  
 11 <141> CURRENT FILING DATE: 2001-12-21  
 13 <150> PRIOR APPLICATION NUMBER: 60/257,073  
 14 <151> PRIOR FILING DATE: 2000-12-21  
 16 <160> NUMBER OF SEQ ID NOS: 18  
 18 <170> SOFTWARE: PatentIn Ver. 2.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 5024  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Murinae gen. sp.  
 25 <400> SEQUENCE: 1

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 28 ggggcgatgg aggcgcggag gacacgacca ggccggcgcc ggcctgcgag ggaagtttcc 180  
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 30 gcgtagggcaa ctacctatc ggcagcagga agctgggaga gggctccttc gccaaaggtgc 300  
 31 gcgaggggct gcacgtgctg acgggagaaa aggtagctat caaggtcatc gataagaaaa 360  
 32 gagccaagaa agacacctac gtcacaaaaa acctgcgtcg agaggggcag atccagcaga 420  
 33 tgatccgaca ccccaacatc acacagctcc tggacatctt ggagacagag aacagctact 480  
 34 acctggtcat ggagctgtgt cctggtggca acctcatgca caagatctac gaaaagaaac 540  
 35 ggttgatga agccgaggcc cgcagataca tccggcaact catctctgcg gtggaacacc 600  
 36 tgcaccgtgc gggggtggtt cacagagact tgaagataga gaatttgcta ctagatgaag 660  
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 38 cggatccatt cagcacacag tgtggcagcc ctgcctatgc tgcgccagaa ctgcttgcca 780  
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 41 tggtaggaaa agcaatgaat cccctgccga cccagctctc cacaggggcc gtcaactttc 960  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,256

DATE: 01/16/2002

TIME: 18:45:02

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Output Set: N:\CRF3\01162002\J032256.raw

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57 ggacactctc ccaggggctg ctgtccggaa gtacctcacc tctccaaact ccactgcatt 1920
58 ccacgctggt ctcttttgcc cacgaagaaa agaacagccc cccgaaagag gagggtgtgt 1980
59 gttcaccgcc tcccgctccc agtaatggcc tcctgcagcc tctggggagc cccaactgtg 2040
60 tgaagagcag gggacggttc cccatgatgg gcctcggaca gatgctgagg aagcggcacc 2100
61 agagcctgca gccttccctca gagaggtccc tggacgccag catgtcccct ctgcagccca 2160
62 tagcccccct cagcctctcc tttgacatgg ccgacggtgt caagggccag tgttaacctg 2220
63 ggatggcaag attctgggtc tctgtgagga cagccacgga acagagctcc acacaggcag 2280
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65 acaaagtccc acgcttgatc cagctgaagt ccacactcaa agtccacgca cttacttagg 2400
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101 tcgagaacag cgtcagatgt acaactagtt tgctgcgtt gctactggta ccttggactc 4560
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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/032,256

DATE: 01/16/2002  
TIME: 18:45:02

Input Set : A:\M2335hn1.app  
Output Set: N:\CRF3\01162002\J032256.raw

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106 tcatgaatga gtctttgcct gtgattctag tcagcctgtg gctactgatg ggaacggccg 4860
107 atctgtcatc atgtgaagtc caggaggaag aatctatctt agtcatacga tttgggtcatg 4920
108 agtaaggact atatttatgt caccactatt gaatatatgt acttttataa tggctgtgaa 4980
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113 <211> LENGTH: 714
114 <212> TYPE: PRT
115 <213> ORGANISM: Murinae gen. sp.
117 <400> SEQUENCE: 2
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121 Gly Gly Asp Gly Ala Glu Asp Thr Arg Pro Ala Ala Cys
122 20 25 30
124 Glu Gly Ser Phe Leu Pro Ala Trp Val Ser Gly Val Ser Arg Glu Arg
125 35 40 45
127 Leu Arg Asp Phe Gln His His Lys Arg Val Gly Asn Tyr Leu Ile Gly
128 50 55 60
130 Ser Arg Lys Leu Gly Glu Gly Ser Phe Ala Lys Val Arg Glu Gly Leu
131 65 70 75 80
133 His Val Leu Thr Gly Glu Lys Val Ala Ile Lys Val Ile Asp Lys Lys
134 85 90 95
136 Arg Ala Lys Lys Asp Thr Tyr Val Thr Lys Asn Leu Arg Arg Glu Gly
137 100 105 110
139 Gln Ile Gln Gln Met Ile Arg His Pro Asn Ile Thr Gln Leu Leu Asp
140 115 120 125
142 Ile Leu Glu Thr Glu Asn Ser Tyr Tyr Leu Val Met Glu Leu Cys Pro
143 130 135 140
145 Gly Gly Asn Leu Met His Lys Ile Tyr Glu Lys Lys Arg Leu Asp Glu
146 145 150 155 160
148 Ala Glu Ala Arg Arg Tyr Ile Arg Gln Leu Ile Ser Ala Val Glu His
149 165 170 175
151 Leu His Arg Ala Gly Val Val His Arg Asp Leu Lys Ile Glu Asn Leu
152 180 185 190
154 Leu Leu Asp Glu Asp Asn Asn Ile Lys Leu Ile Asp Phe Gly Leu Ser
155 195 200 205
157 Asn Cys Ala Gly Ile Leu Gly Tyr Ser Asp Pro Phe Ser Thr Gln Cys
158 210 215 220
160 Gly Ser Pro Ala Tyr Ala Ala Pro Glu Leu Leu Ala Arg Lys Lys Tyr
161 225 230 235 240
163 Gly Pro Lys Ile Asp Val Trp Ser Ile Gly Val Asn Met Tyr Ala Met
164 245 250 255
166 Leu Thr Gly Thr Leu Pro Phe Thr Val Glu Pro Phe Ser Leu Arg Ala
167 260 265 270
169 Leu Tyr Gln Lys Met Val Asp Lys Ala Met Asn Pro Leu Pro Thr Gln
170 275 280 285
172 Leu Ser Thr Gly Ala Val Asn Phe Leu Arg Ser Leu Leu Glu Pro Asp

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/032,256

DATE: 01/16/2002

TIME: 18:45:02

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Output Set: N:\CRF3\01162002\J032256.raw

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175 Pro Val Lys Arg Pro Asn Ile Gln Gln Ala Leu Ala Asn Arg Trp Leu
176 305      310      315      320
178 Asn Glu Asn Tyr Thr Gly Lys Val Pro Cys Asn Val Thr Tyr Pro Asn
179      325      330      335
181 Arg Ile Ser Leu Glu Asp Leu Ser Pro Ser Val Val Leu His Met Thr
182      340      345      350
184 Glu Lys Leu Gly Tyr Lys Asn Ser Asp Val Ile Asn Thr Val Leu Ser
185      355      360      365
187 Asn Arg Ala Cys His Ile Leu Ala Ile Tyr Phe Leu Leu Asn Lys Lys
188      370      375      380
190 Leu Glu Arg Tyr Leu Ser Gly Lys Ser Asp Ile Gln Asp Ser Ile Cys
191 385      390      395      400
193 Tyr Lys Thr Gln Leu Tyr Gln Ile Glu Lys Cys Arg Ala Thr Lys Glu
194      405      410      415
196 Pro Tyr Glu Ala Ser Leu Asp Thr Trp Thr Arg Asp Phe Glu Phe His
197      420      425      430
199 Ala Val Gln Asp Lys Lys Pro Lys Glu Gln Glu Lys Arg Gly Asp Phe
200      435      440      445
202 Leu His Arg Pro Phe Ser Lys Lys Leu Asp Lys Asn Leu Pro Ser His
203      450      455      460
205 Lys Gln Pro Ser Pro Ser Leu Ile Thr Gln Leu Gln Ser Thr Lys Ala
206 465      470      475      480
208 Leu Leu Lys Asp Arg Lys Ala Ser Lys Ser Gly Phe Pro Asp Lys Asp
209      485      490      495
211 Ser Phe Val Cys Arg Asn Leu Phe Arg Lys Thr Ser Asp Ser Asn Cys
212      500      505      510
214 Val Ala Ser Ser Ser Met Glu Phe Ile Pro Val Pro Pro Arg Thr
215      515      520      525
217 Pro Arg Ile Val Lys Lys Leu Glu Pro His Gln Pro Gly Pro Gly Ser
218      530      535      540
220 Ala Ser Ile Leu Pro Lys Glu Glu Pro Leu Leu Leu Asp Met Val Arg
221 545      550      555      560
223 Ser Phe Glu Ser Val Asp Arg Glu Asp His Ile Glu Leu Leu Ser Pro
224      565      570      575
226 Ser His His Tyr Arg Ile Leu Ser Ser Pro Val Ser Leu Ala Arg Arg
227      580      585      590
229 Asn Ser Ser Glu Arg Thr Leu Ser Gln Gly Leu Leu Ser Gly Ser Thr
230      595      600      605
232 Ser Pro Leu Gln Thr Pro Leu His Ser Thr Leu Val Ser Phe Ala His
233      610      615      620
235 Glu Glu Lys Asn Ser Pro Pro Lys Glu Glu Gly Val Cys Ser Pro Pro
236 625      630      635      640
238 Pro Val Pro Ser Asn Gly Leu Leu Gln Pro Leu Gly Ser Pro Asn Cys
239      645      650      655
241 Val Lys Ser Arg Gly Arg Phe Pro Met Met Gly Ile Gly Gln Met Leu
242      660      665      670
244 Arg Lys Arg His Gln Ser Leu Gln Pro Ser Ser Glu Arg Ser Leu Asp
245      675      680      685

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DATE: 01/16/2002  
TIME: 18:45:02

Input Set : A:\M2335hn1.app  
Output Set: N:\CRF3\01162002\J032256.raw

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250 Asp Met Ala Asp Gly Val Lys Gly Gln Cys  
251 705 710  
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255 <211> LENGTH: 10  
256 <212> TYPE: RNA  
257 <213> ORGANISM: Unknown Organism  
259 <220> FEATURE:  
260 <223> OTHER INFORMATION: Description of Unknown Organism:Kozak consensus  
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264 gccrccaugg 10  
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269 <212> TYPE: DNA  
270 <213> ORGANISM: Unknown Organism  
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274 signal  
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277 aataaa 6  
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281 <211> LENGTH: 6  
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283 <213> ORGANISM: Murinae gen. sp.  
285 <400> SEQUENCE: 5  
286 aataca 6  
289 <210> SEQ ID NO: 6  
290 <211> LENGTH: 6  
291 <212> TYPE: PRT  
292 <213> ORGANISM: murine Hunk;fragment  
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296 1 5  
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300 <211> LENGTH: 21  
301 <212> TYPE: DNA  
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304 <220> FEATURE:  
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306 oligonucleotide primer PTKIa  
308 <400> SEQUENCE: 7  
309 gggccccggat ccacmngay y) see item 9 on Eva summary sh  
312 <210> SEQ ID NO: 8  
313 <211> LENGTH: 28  
314 <212> TYPE: DNA  
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317 <220> FEATURE:

W-->

→ see item 9 on Ena summary sheet

21

## VERIFICATION SUMMARY

DATE: 01/16/2002

PATENT APPLICATION: US/10/032,256

TIME: 18:45:03

Input Set : A:\M2335hn1.app

Output Set: N:\CRF3\01162002\J032256.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:309 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7  
L:309 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7  
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7